

37 C.F.R. §1.121(h). The fees required pursuant to 37 C.F.R. §1.16(e) and 37 C.F.R. §1.492(f) have been submitted previously.

IN THE SPECIFICATION

Please **delete** the Sequence Listing presently of record and substitute, therefor, the attached Substitute Sequence Listing.

Please **amend** the paragraph beginning on page 4, line 14 (of the English translation) and ending on page 4, line 18 with the following rewritten paragraph:

Description of the Sequence Listing

SEQ ID NO:1: *SGS3* gene of *Arabidopsis thaliana*.
SEQ ID NO:2: cDNA of the *SGS3* gene of *Arabidopsis thaliana*.
SEQ ID NO:3: *SGS3* polypeptide of *Arabidopsis thaliana*.
SEQ ID NO:4: Primer p356AD'.
SEQ ID NO:5: Primer p356Y'.

Please **amend** the paragraph beginning on page 47, line 1 (of the English translation) and ending on page 47, line 22 with the following rewritten paragraph:

The DNA sequence which was inserted at the BamHI site of the pBin+ plasmid and which had led to the isolation of the bacterial strain 356 was determined. Subclones of the 356 clone were produced in the pBin+ vector and the same *sgs3-2 2a3* line was transformed with these subclones in order to determine those

capable of restoring the function of the *SGS3* gene. The smallest subclone capable of restoring this function constitutes the *SGS3* gene such as it is described in this disclosure. It was possible to predict the ORF of *SGS3* by computer analysis. The sequence of the cDNA containing the ORF of the *SGS3* gene, and therefore the position of the promoter, terminator and intronic sequences of *SGS3*, were verified after having isolated and cloned this sequence. In order to isolate, we first performed a reverse transcription reaction using *Arabidopsis thaliana* total RNA. We then performed a PCR reaction on this pool of cDNA using the pair of primers p356AD' (AAAATGAGTTCTAGGGCTGGTCC; SEQ ID NO:4) and p356Y' (GTCTCAATCATCTTCATTGTGAAGGCC; SEQ ID NO:5). These primers are located at the 2 ends of the ORF of *SGS3*. This PCR product was cloned and sequenced.

IN THE CLAIMS

Please **cancel** claims 1-22.

Please **add** the following new claims:

23. (NEW) An isolated nucleic acid comprising a nucleotide sequence having at least 80% homology to a reference nucleotide sequence wherein the reference sequence is selected